

BLAST Basic Local Alignment Search Tool**Job Title: Nucleotide sequence (21 letters)**

- Your search parameters were adjusted to search for a short input sequence.

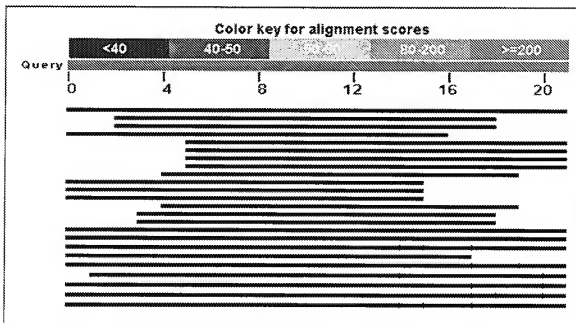
Please, try our new design!

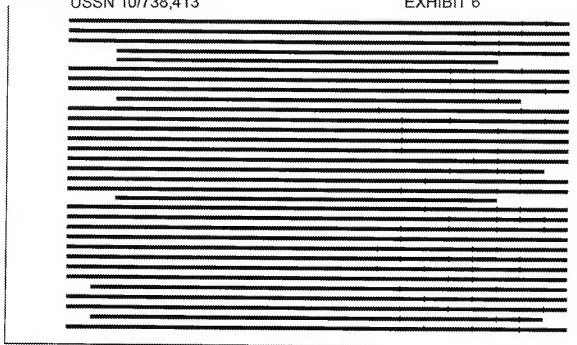
BLASTN 2.2.18+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402. RID: 9HCHHWH3015 **Database:** human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters

Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= Length=21

 Designing or Testing PCR Primers? Try your s**Distribution of 1401 Blast Hits on the Query Sequence**



Message: Draw of results NEW

Legend for links to other resources: UniGene GEO Gene Structure Map

Sequences producing significant alignments:

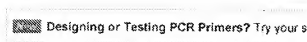
(Click headers to sort columns)

Transcripts

gi 113722118 NM_000372.4	Homo sapiens tyrosinase (oculocutaneous albinism IA) (TYR), mRNA	42.1	42.1	100%	0.005	100%	
gi 148806860 NR_003571.1	Homo sapiens protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) pseudogene (LOC728758) on chromosome 15	32.2	32.2	76%	4.7	100%	
gi 4809273 NM_001154.2	Homo sapiens annexin A5 (ANXA5), mRNA	32.2	32.2	76%	4.7	100%	
gi 14150142 NM_032347.1	Homo sapiens zinc finger protein 397 (ZNF397), mRNA	32.2	32.2	76%	4.7	100%	
gi 65508003 NM_024426.3	Homo sapiens Wilms tumor 1 (WT1), transcript variant D, mRNA	32.2	32.2	76%	4.7	100%	
gi 65507907 NM_024425.2	Homo sapiens Wilms tumor 1 (WT1), transcript variant C, mRNA	32.2	32.2	76%	4.7	100%	
gi 65507816 NM_024424.2	Homo sapiens Wilms tumor 1 (WT1), transcript variant B, mRNA	32.2	32.2	76%	4.7	100%	
gi 65507713 NM_000378.3	Homo sapiens Wilms tumor 1 (WT1), transcript variant A, mRNA	32.2	32.2	76%	4.7	100%	
gi 98986451 NM_023075.4	Homo sapiens metallophosphoesterase 1 (MPPE1), mRNA	30.2	30.2	71%	19	100%	
gi 46488931 NM_000629.2	Homo sapiens interferon (alpha, beta and omega) receptor 1 (IPNAR1), mRNA	30.2	30.2	71%	19	100%	
gi 62388889 NM_001014797.1	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), transcript variant 1, mRNA	30.2	30.2	71%	19	100%	
gi 26638649 NM_002247.2	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), transcript variant 2, mRNA	30.2	30.2	71%	19	100%	
gi 24307982 NM_015050.1	Homo sapiens KIAA0082 (KIAA0082), mRNA	30.2	30.2	71%	19	100%	
gi 56549110 NM_001008213.1	Homo sapiens optineurin (OPTN), transcript variant 4, mRNA	30.2	30.2	71%	19	100%	
gi 56549108 NM_001008212.1	Homo sapiens optineurin (OPTN), transcript variant 3, mRNA	30.2	30.2	71%	19	100%	

Genomic sequences [show first]

gi 157812179 NW_001838029.2	Homo sapiens chromosome 11	42.1	122	100%	0.005	100%
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Alignments

>gi|113722118|ref|NM_000372.4| **UEGM** Homo sapiens tyrosinase (oculocutaneous albinis
Length=2082

GENE ID: 7299 TYR | tyrosinase (oculocutaneous albinism IA) [Homo sapiens]
(Over 100 PubMed links)

Score = 42.1 bits (21), Expect = 0.005
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

Query 1 AATCCTGGAAACCATGACAAA 21
Sbjct 980 AATCCTGGAAACCATGACAAA 1000

>gi|148806860|ref|NR_003571.1| **GM** Homo sapiens protein (peptidylprolyl cis/trans isom
4 (parvulin) pseudogene (LOC728758) on chromosome
15
Length=2366

GENE ID: 728758 hCG_1789710 | protein (peptidylprolyl cis/trans isomerase)
NIMA-interacting, 4 (parvulin) pseudogene [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 4.7
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 TCCTGGAAACCATGAC 18
Sbjct 252 TCCTGGAAACCATGAC 237

>gi|4809273|ref|NM_001154.2| **UEGM** Homo sapiens annexin A5 (ANXA5), mRNA
Length=1630

Score = 32.2 bits (16), Expect = 4.7
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 TCCTGGAAACCATGAC 18
Sbjct 1021 TCCTGGAAACCATGAC 1006

>gi|14150142|ref|NM_032347.1| **UEGM** Homo sapiens zinc finger protein 397 (ZNF397), m
Length=1439

GENE ID: 84307 ZNF397 | zinc finger protein 397 [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 4.7

USSN 10/738,413

EXHIBIT 6

Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AATCCTGGAAACCATG 16
Sbjct 659 AATCCTGGAAACCATG 674

>gi|65508003|ref|NM_024426.3| **UEGM** Homo sapiens Wilms tumor 1 (WT1), transcript var
Length=3029

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21
Sbjct 2192 TGGAAACCATGACAAA 2177

>gi|65507907|ref|NM_024425.2| **UEGM** Homo sapiens Wilms tumor 1 (WT1), transcript var
Length=2978

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21
Sbjct 2141 TGGAAACCATGACAAA 2126

>gi|65507816|ref|NM_024424.2| **UEGM** Homo sapiens Wilms tumor 1 (WT1), transcript var
Length=3020

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21
Sbjct 2183 TGGAAACCATGACAAA 2168

>gi|65507713|ref|NM_000378.3| **UEGM** Homo sapiens Wilms tumor 1 (WT1), transcript var
Length=2969

GENE ID: 7490 WT1 | Wilms tumor 1 [Homo sapiens] (Over 100 PubMed links)

Score = 32.2 bits (16), Expect = 4.7
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 6 TGGAAACCATGACAAA 21
Sbjct 2132 TGGAAACCATGACAAA 2117

>gi|98986451|ref|NM_023075.4| **UEGM** Homo sapiens metallophosphoesterase 1 (MPPE1), m
Length=2806

GENE ID: 65258 MPPE1 | metallophosphoesterase 1 [Homo sapiens]
(10 or fewer PubMed links)

Score = 30.2 bits (15), Expect = 19

Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 5 CTGGAAACCATGACA 19
Sbjct 1105 CTGGAAACCATGACA 1119